GENOMIC CHARACTERIZATION AND GENE REGULATION OPTIMIZATION TO FURTHER IMPROVE AN ENZYMATIC MIX USED AS FEED ADDITIVE

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A common indigestible fraction of cereal grains, representing a large part of poultry diet, is their content in non-starch polysaccharides (NSP). *Talaromyces versatilis* is a filamentous fungus presenting the capability to secrete a mixture of enzymes used as animal feed additive (Rovabio® Excel) to enhance hydrolysis of plant cell wall polysaccharides. When incorporated to feed, the nutrients are more efficiently digested leading to a decreased need in agricultural products and hence a more sustainable production of poultry meat. In this context, the genome of *T. versatilis* was sequenced and annotated with a focus on genes likely to encode glycoside hydrolases, transcription factors and proteins involved in the secretion pathway. We also undertook a genome-wide transcriptome analysis, of the fungus exposed to glucose or milled wheat straw (a complex lignocellulosic material), using RNA-seq. The data revealed that, incubated on glucose and then transferred to wheat straw, the mycellium expressed differentially 926 genes between the two conditions. The differential response in gene expression of key mutants such as *⊿xlnR, ⊿creA* or *⊿araR* were analysed in order to study their roles in regulating transcription. This approach provides a global view of the network that regulates the expression of the glycoside hydrolyse-encoding genes. More specifically, XlnR was identified as the transcription factor controling expression of genes involved in arabinoxylan degradation. Within the variety of NSP, arabinoxylan is the prominent type for wheat and corn (around 50%). Despite being mainly composed of xylose (X) and arabinose (A), the A:X ratio are different between corn and wheat, with a higher value for corn and a higher proportion of substituted xyloses compared to wheat. Arabinofuranosidase activity enhancement is key to attack arabinoxylans with a high A:X ratio which are recalcitrant to breakdown by single xylanase activity. Therefore, we aimed at improving the Rovabio® Excel in order to improve its capacity to degrade highly branched arabinoxylans, by enriching it in arabinofuranosidases and xylanases. To address such a goal while keeping its enzymatic diversity, we over-expressed the XlnR transcription factor. As a result, we obtained a modified strain of *Talaromyces versatilis* with on optimized genetic regulation to secrete a higher amount of arabinoxylan degrading enzymes. The resulting product, named Rovabio® Advance, tested in broilers allowed restoring nutrient availability, and so growth performance, even with a nutrient content diluted by 3% compared to a control diet.